

## SEQUENCE LISTING

<110> THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
 AURORA BIOSCIENCES CORPORATION  
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 CUBITT, Andrew

<120> TANDEM FLUORESCENT PROTEIN CONSTRUCTS

<130> REGEN1260-3

<150> US 08/792,553

<151> 1997-01-31

<150> US 09/396,003

<151> 1999-09-13

<160> 31

<170> PatentIn version 3.1

<210> 1

<211> 716

<212> DNA

<213> Aequorea victoria

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<221> CDS

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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
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gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	

ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	

act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	

tct tat ggt gtt caa tgc ttt tca aga tac cca gat cat atg aaa cgg	240
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	

cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	

act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa gtc	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	

aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att	384
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Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125  
 gat ttt aaa gaa gat gga aac att ctt gga cac aaa ttg gaa tac aac 432  
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140  
 tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat gga 480  
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly  
 145 150 155 160  
 atc aaa gtt aac ttc aaa att aga cac aac att gaa gat gga agc gtt 528  
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val  
 165 170 175  
 caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc cct 576  
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
 180 185 190  
 gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt tcg 624  
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
 195 200 205  
 aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt gta 672  
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
 210 215 220  
 aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa ta 716  
 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
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 20 25 30  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

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Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly  
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val  
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
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Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
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Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
 225 230 235

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Ser Gln Asn Tyr Pro Ile Val Gly  
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Pro Ser Pro Arg Glu Gly Lys Arg Ser Tyr  
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Tyr Val Ala Asp Gly  
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Met Phe Gly Gly Ala Lys Lys Arg  
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Gly Val Val Asn Ala Ser Ser Arg Leu Ala  
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Leu Ile Ala Tyr Leu Lys Lys Ala Thr  
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Val Lys Met Asp Ala Glu Phe  
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Phe Leu Ala Glu Gly Gly Gly Val Arg Gly Pro Arg Val Val Glu Arg  
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His

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Asp Arg Val Tyr Ile His Pro Phe His Leu Val Ile His  
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<210> 13

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<211> 8  
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<400> 13

Lys Pro Ala Leu Phe Phe Arg Leu  
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<210> 14  
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<400> 14

Gln Pro Leu Gly Gln Thr Ser Leu Met Lys Arg Pro Pro Gly Phe Ser  
 1 5 10 15

Pro Phe Arg Ser Val Gln Val Met Lys Thr Gln Glu Gly Ser  
 20 25 30

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Gly Gly Gly Gly Ser  
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<400> 16

Gly Gly Gly Gly Gly Gly Ser Met Phe Gly Gly Ala Lys Lys Arg Ser  
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Gly Gly Gly Gly Gly Gly  
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<400> 17

Ile Gln Arg Met Lys Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser  
 1 5 10 15

Lys Asn Tyr His Leu Glu Asn Glu Val Ala Arg Leu Lys Lys Leu Val  
 20 25 30

Gly Glu Arg  
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<400> 18

Ser Lys Val Ile Leu Phe  
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<210> 19  
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<400> 19  
 ggatccccc gctgaattca tg

22

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 aaataataag gatcc

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<400> 22  
 agaaaggcta gcaaaggaga agaa 24

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<400> 23  
 tcagtctaga tttgtatagt tcata 25

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<220>  
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<400> 24

Met Arg Gly Ser His His His His His His  
 1 5 10

<210> 25  
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<220>  
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<400> 25



Ser Ser Met Thr Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp  
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Asp Asp Lys Asp Pro Pro Ala Glu Phe  
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<210> 26  
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<400> 26

Ala Asn Pro Leu Tyr Lys Asp Ala Thr Asp Phe Thr  
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<210> 27  
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<400> 27

Thr Ala Asn Pro Leu Tyr Lys Asp Ala Thr Ser Asp Phe Thr  
 1 5 10

<210> 28  
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 <212> PRT  
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<400> 28

Gly Thr Ala Asn Pro Leu Tyr Lys Asp Ala Thr Ser Gly Asp Phe Thr  
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<210> 29  
 <211> 18  
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<400> 29

Gly Thr Ala Asn Pro Leu Tyr Lys Asp Ala Thr Ser Gly Ser Thr Asp

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5

10

15

Phe Thr

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&lt;211&gt; 20

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&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Linker sequence

&lt;400&gt; 30

Gly	Thr	Ala	Asn	Pro	Leu	Tyr	Lys	Asp	Ala	Thr	Ser	Gly	Ser	Thr	Gly
1				5				10					15		

Ser	Asp	Phe	Thr
			20

&lt;210&gt; 31

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Linker sequence

&lt;400&gt; 31

Gly	Thr	Ala	Asn	Pro	Leu	Tyr	Lys	Asp	Ala	Thr	Ser	Gly	Ser	Thr	Gly
1				5				10					15		

Ser	Gly	Ser	Asp	Phe	Thr
					20

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